1.Application No.: 09/129,958

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s)

☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other

OCT 1 8 1999

Applicant Must Provide:

☒ An _initial_ or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An _initial_ or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE
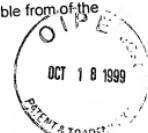
Friedman

RAW SEQUENCE LISTING
ERROR REPORT
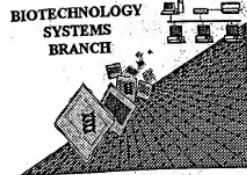
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/129,958

Art Unit / Team No. : 1655

Date Processed by STIC: 7/20/99

OIPE

OCT 18 1999

PATENT : BRANCH

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-30°-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: _09/129958_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid
        Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ Patentin ver. 2.0 "bug"

A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, Patentin would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences
        (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences
        (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's
         (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism
         (NEW RULES)

Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature
         (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ Patentin ver. 2.0 "bug"

Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

This Raw Listing contains the General Information
Section and up to first 5 pages.   Does Not Comply
                                    Corrected Diskette Needed

pp 1-2

```
1    <110> APPLICANT: Mills, Allen P.
2          Yurke, Bernard
3          Platzman, Philip M.
4    <120> TITLE OF INVENTION: ANALOG AND NEURAL NETWORK COMPUTATION USING DNA
5    <130> FILE REFERENCE: LUTEC 0008
6    <140> CURRENT APPLICATION NUMBER: US/09/129,958
7    <141> CURRENT FILING DATE: 1998-08-06
8    <150> EARLIER APPLICATION NUMBER: 09/078,761
9    <151> EARLIER FILING DATE: 1998-05-15
10   <150> EARLIER APPLICATION NUMBER: 09/018,248
11   <151> EARLIER FILING DATE: 1998-02-03
12   <150> EARLIER APPLICATION NUMBER: 60/086,654
13   <151> EARLIER FILING DATE: 1998-05-26
14   <160> NUMBER OF SEQ ID NOS: 4
15   <170> SOFTWARE: PatentIn Ver. 2.0
16   <210> SEQ ID NO 1
17   <211> LENGTH: 10
18   <212> TYPE: DNA
19   <213> ORGANISM: Artificial Sequence
20   <220> FEATURE:
21   <223> OTHER INFORMATION: Description of Artificial Sequence:  DNA based
22         analog oligonucleotide
23   <400> SEQUENCE: 1                                              10
24         agctatcgat
25   <210> SEQ ID NO 2
26   <211> LENGTH: 34
27   <212> TYPE: DNA
28   <213> ORGANISM: Artificial Sequence
29   <220> FEATURE:
30   <223> OTHER INFORMATION: Description of Artificial Sequence:  DNA based
31         analog oligonucleotide
32   <220> FEATURE:
33   <221> NAME/KEY: variation
34   <222> LOCATION: (34)
35   <400> SEQUENCE: 2                                                   34
36         aatgcaagat cgaaatttat acgtttatct tacn
37   <210> SEQ ID NO 3
38   <211> LENGTH: 34
39   <212> TYPE: DNA
40   <213> ORGANISM: Artificial Sequence
41   <220> FEATURE:
42   <223> OTHER INFORMATION: Description of Artificial Sequence:  DNA based
43         analog oligonucleotide
44   <220> FEATURE:
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W-->

an explanation of "n" is mandatory in <2237 response
(see item 10 on Exam Summary sheet and see 1.823 f sequence Rules,

1655

DATE: 07/20/1999
TIME: 16:36:07

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/129,958

PAGE: 2

Input Set: **I129958.RAW**

```
45   <221> NAME/KEY: variation                    same error
46   <222> LOCATION: (34)
47   <400> SEQUENCE: 3                                                    34
48         aatgcaagat cgaaatttat acgtttatct tac n
W-->
49   <210> SEQ ID NO 4
50   <211> LENGTH: 30
51   <212> TYPE: DNA
52   <213> ORGANISM: Artificial Sequence
53   <220> FEATURE:
54   <223> OTHER INFORMATION: Description of Artificial Sequence:  DNA based
55         analog oligonucleotide
56   <400> SEQUENCE: 4                                                    30
57         aatgcaagat cgaaatttat acgtttatct
```

VERIFICATION SUMMARY

PAGE: 3

PATENT APPLICATION US/09/129,958

DATE: 07/20/1999
TIME: 16:36:07

Input Set: I129958.RAW

```
                                                     Original Text
Line  ? Error/Warning                                ------------------------------------------
----- - ------------------------------------------   aatgcaagat cgaaatttat acgtttatct tacn
   36 W "N" or "Xaa" used: Feature required          aatgcaagat cgaaatttat acgtttatct tacn
   48 W "N" or "Xaa" used: Feature required
```